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1 GTTTTCAAAA TCGGTGGAGG TGCATGAAAA AGTTATTGGG CATTTTTTGA AAATAAAAAA
 61 ATATCAATAA GTTGGAGTCA TTACCGAATT TTTATACTTA TTGTTTTAGA ATGAACTTTA
 121 TAACATAGTT GGATAGAGTT TTCGATTAA TACATTAAAT GTGAACCTTG CTACAACAAG
 181 ATGTGCATCA GAAGGAGTGG TTTAATAATC --sarR--TAA
 Ribosomal binding site

[SEQ. I.D. No. 1]

FIG. 1B

| | | | | | |
|------|---|----|----|----|-----|
| | 10 | 20 | 30 | 40 | 50 |
| SarR | M--SKINDINDLVNATFQVKKFFRDTKKKFNLNYEEIYILNHILRSESNEISSKELAKCS | | | | |
| SarA | MAITKINDCFELLSMVTYADKLKSLIKKEFSISFEFAVLTYISENKEKEYYLKDIINHL | | | | |
| | 60 | 70 | 80 | 90 | 100 |
| SarR | EFKPYLTKALQKLKDLKLLSQKRILQDERTVIVVYV-----DTLKHNIHKLISELEE | | | | |
| SarA | NYKQPQVVKAVKILSQEDYFDKKRNEHDERTVLILVNAQQRKKIESLLSRVNRKRITEANN | | | | |

SarR YIKN
 SarA EIEL

SarR = SEQ I.D. No. 2
 SarA = SEQ I.D. No. 3

FIG. 1C

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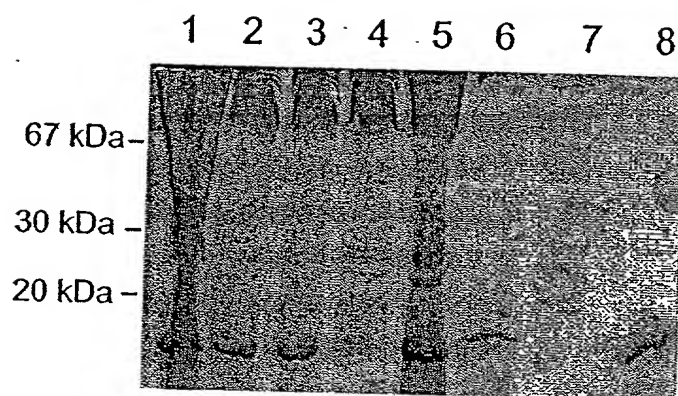


FIG. 2

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FIG. 3A PCR

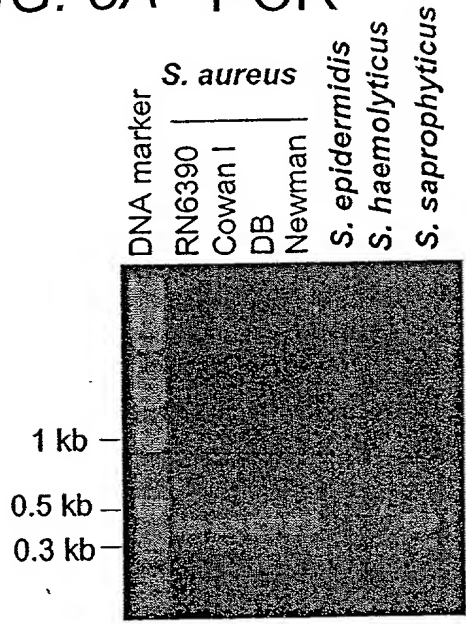


FIG. 3B Southern

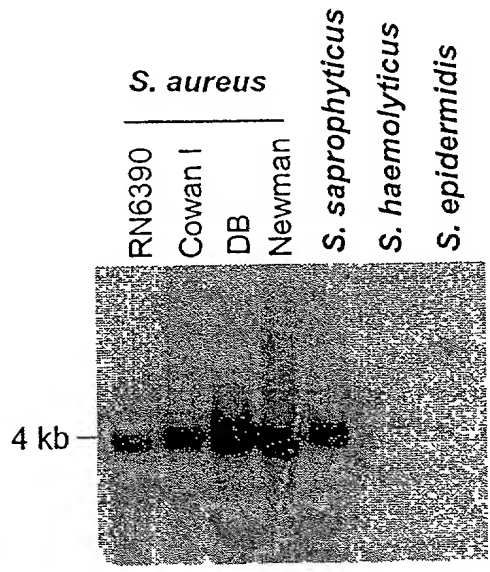


FIG. 3C Northern

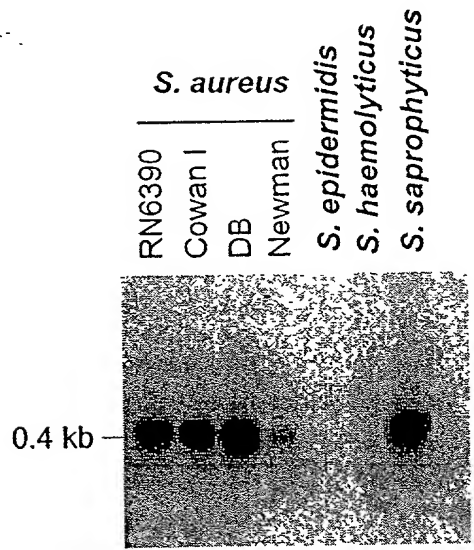
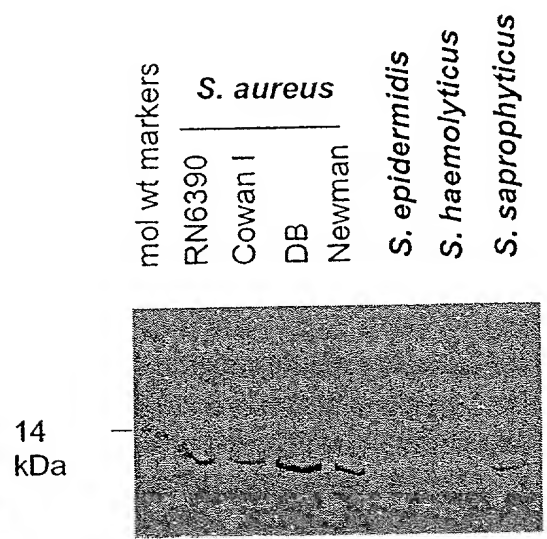


FIG. 3D Immunoblot



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FIG. 4A

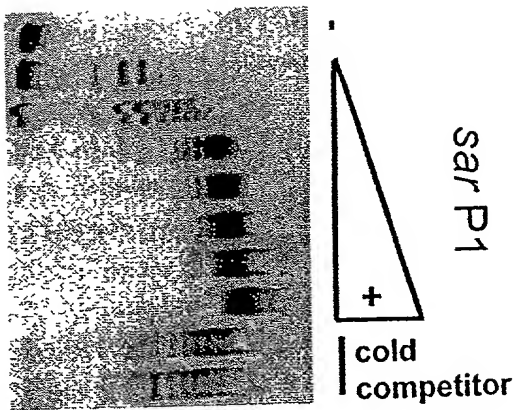


FIG. 4B

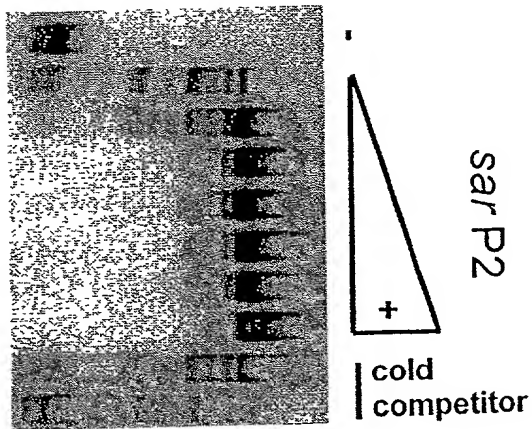
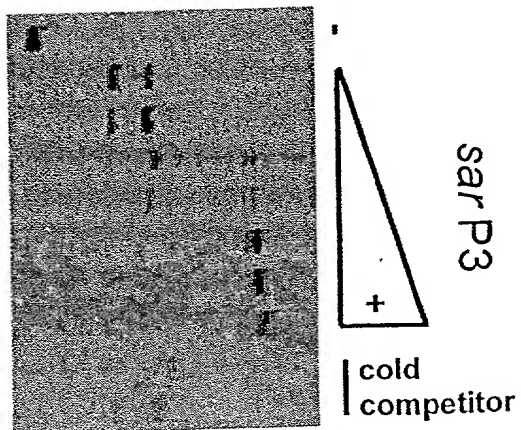


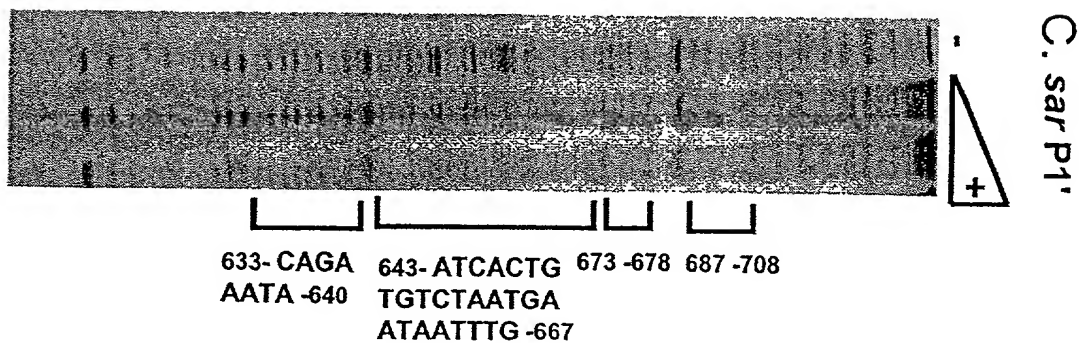
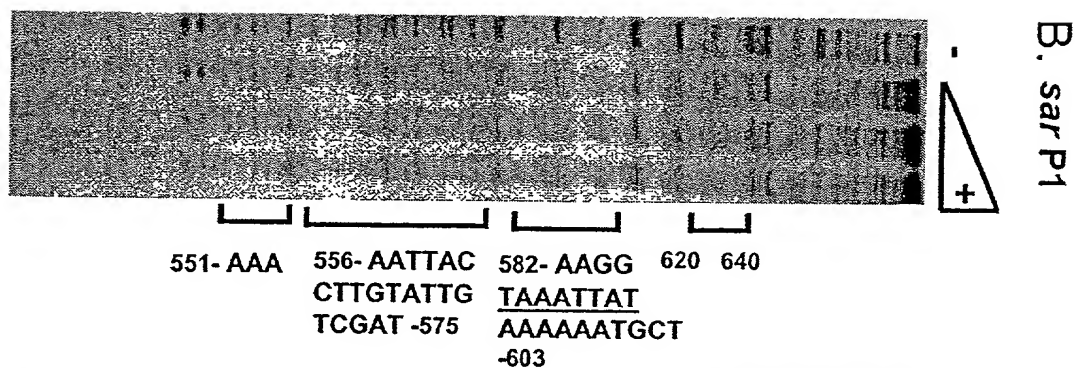
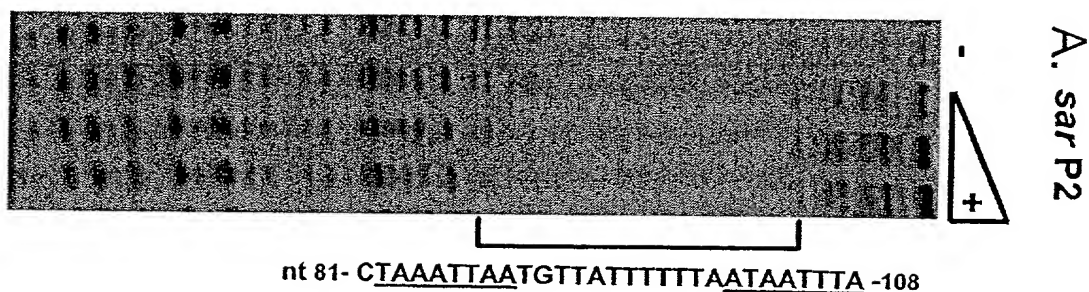
FIG. 4C



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FIG. 5



10043035.01100

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FIG. 6A

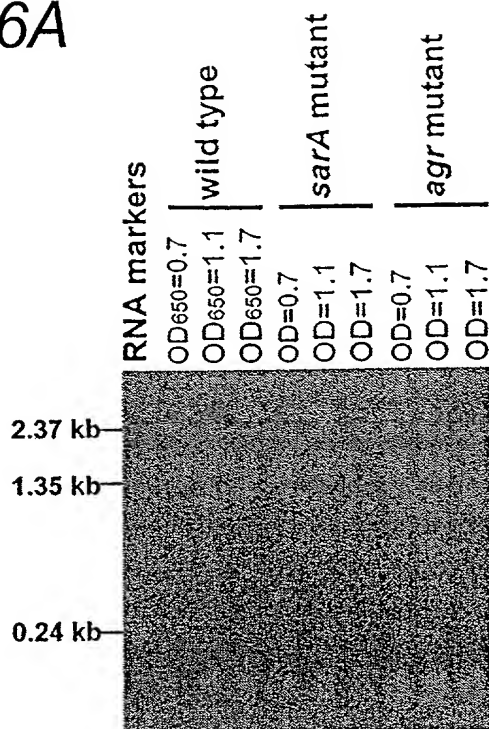


FIG. 6B

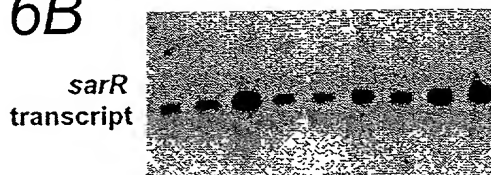


FIG. 6C

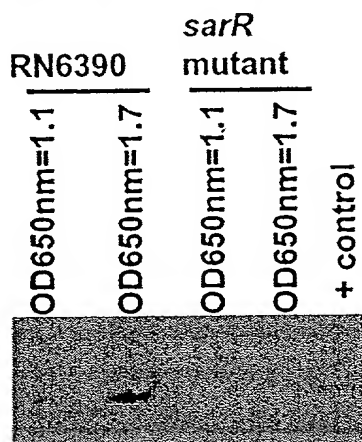


FIG. 7A

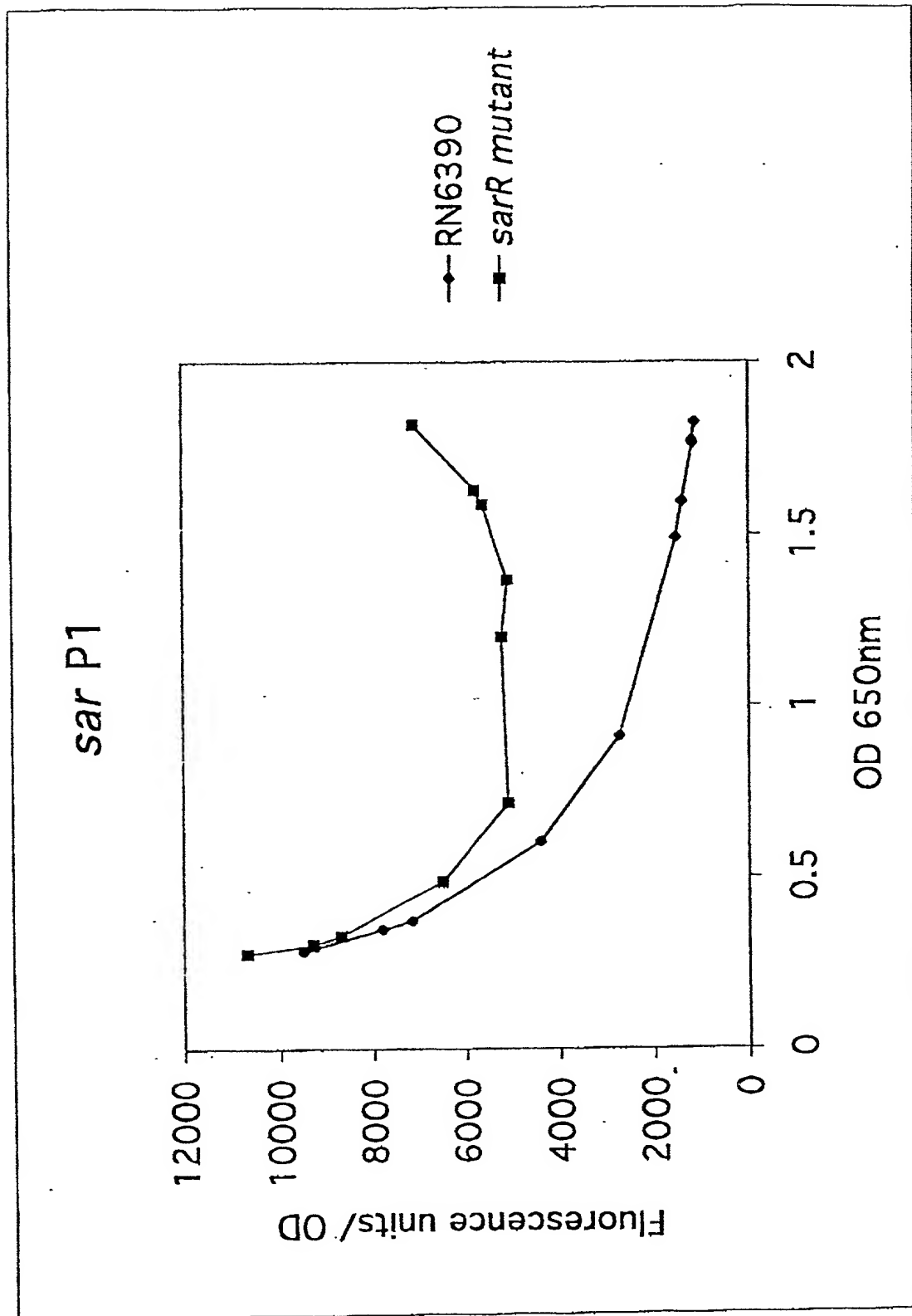
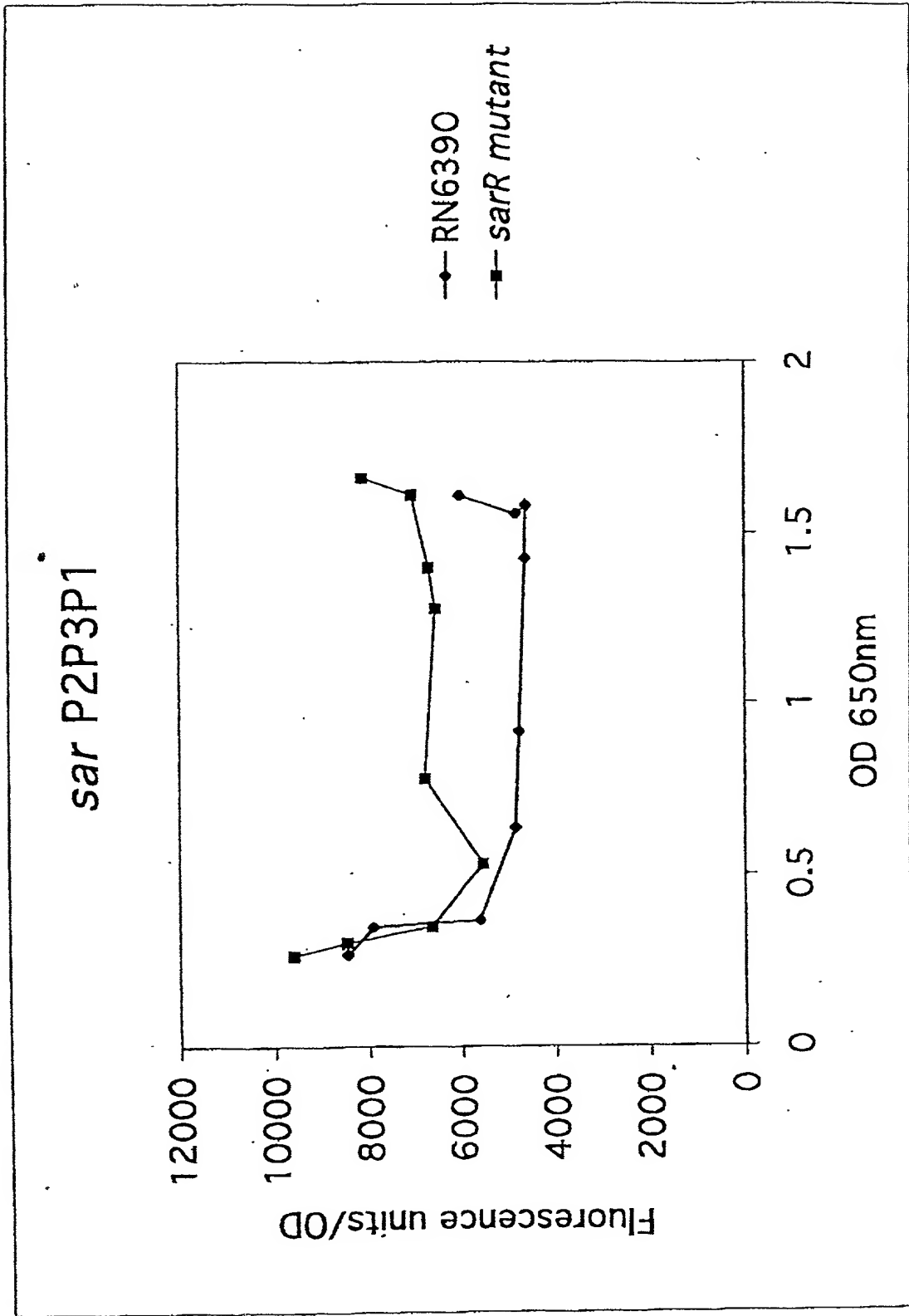


FIG. 7B



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FIG. 8A: *sar* probe

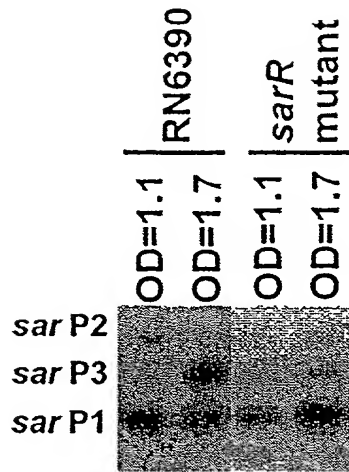


FIG. 8B: anti-SarA antibody

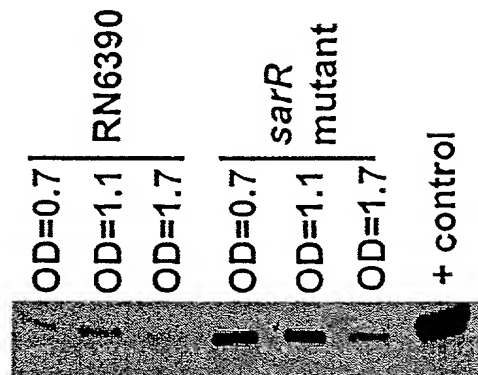
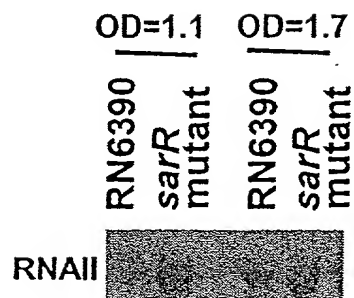


FIG. 8C: *agrA* probe



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FIG. 9A

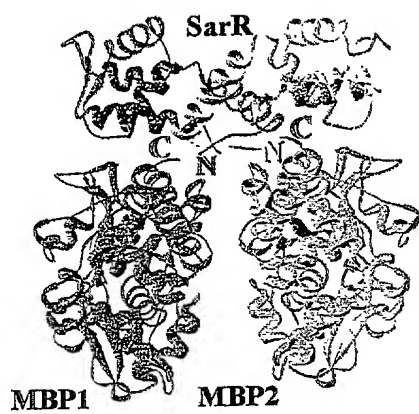


FIG. 9B

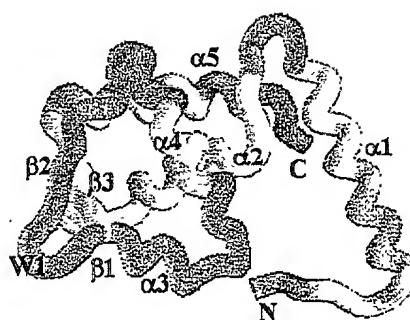


FIG. 10A

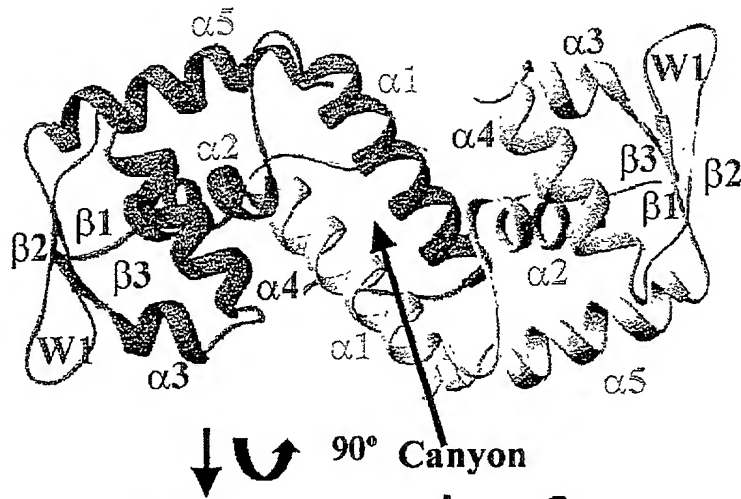


FIG. 10B

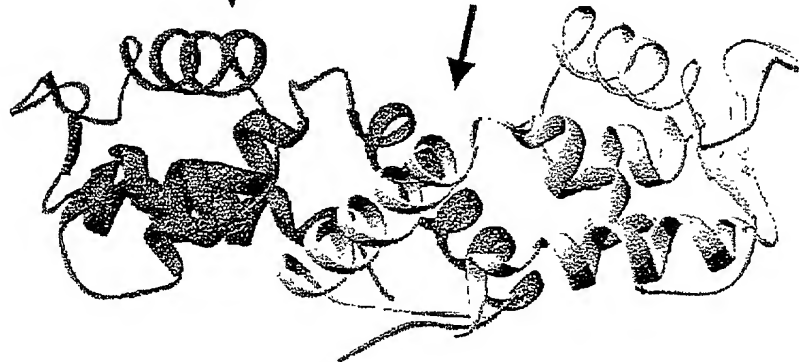
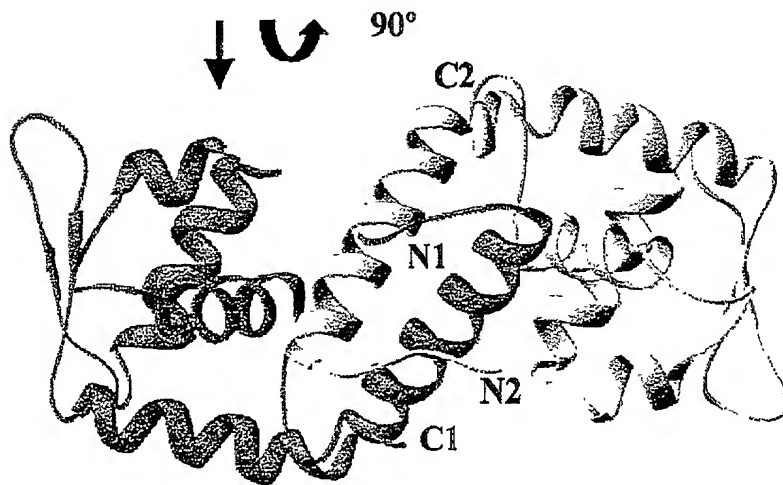
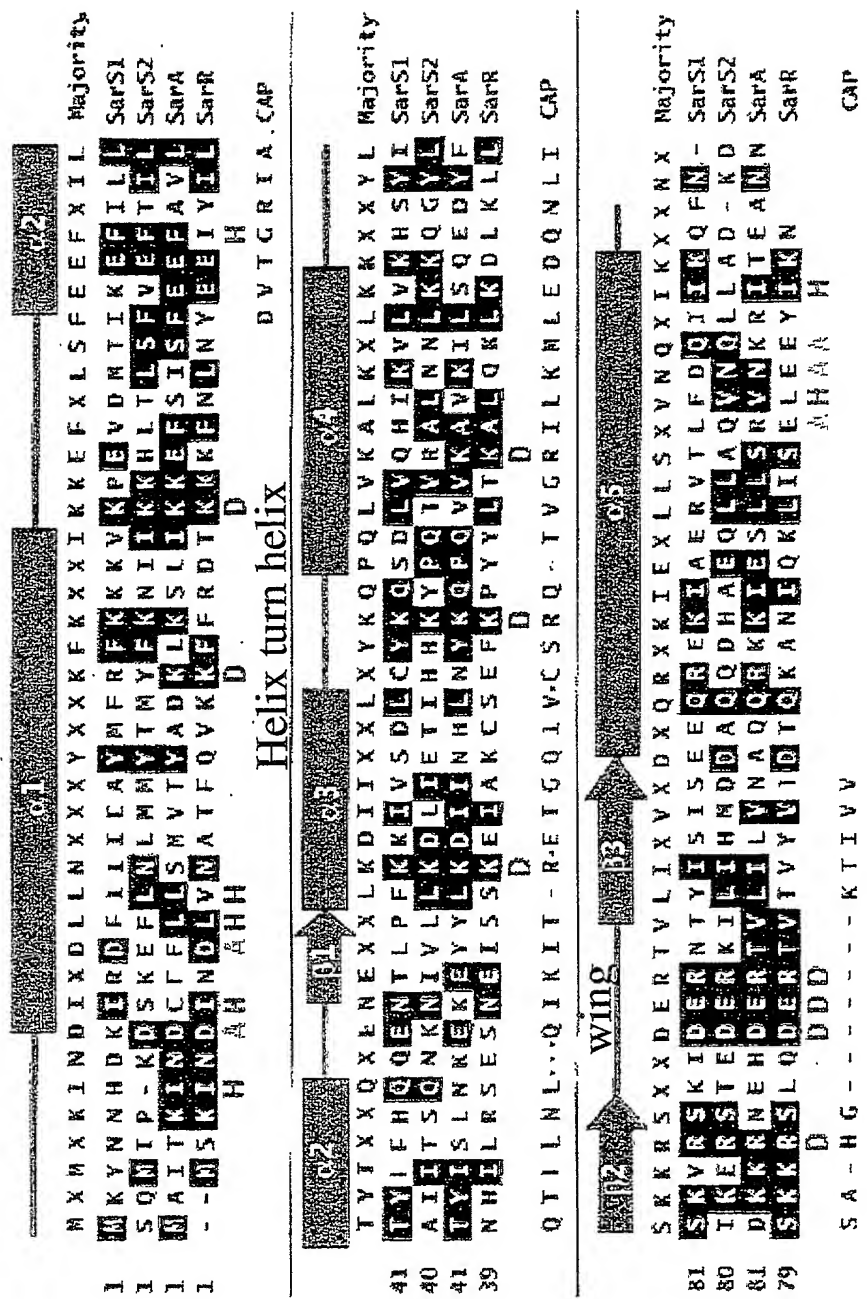


FIG. 10C



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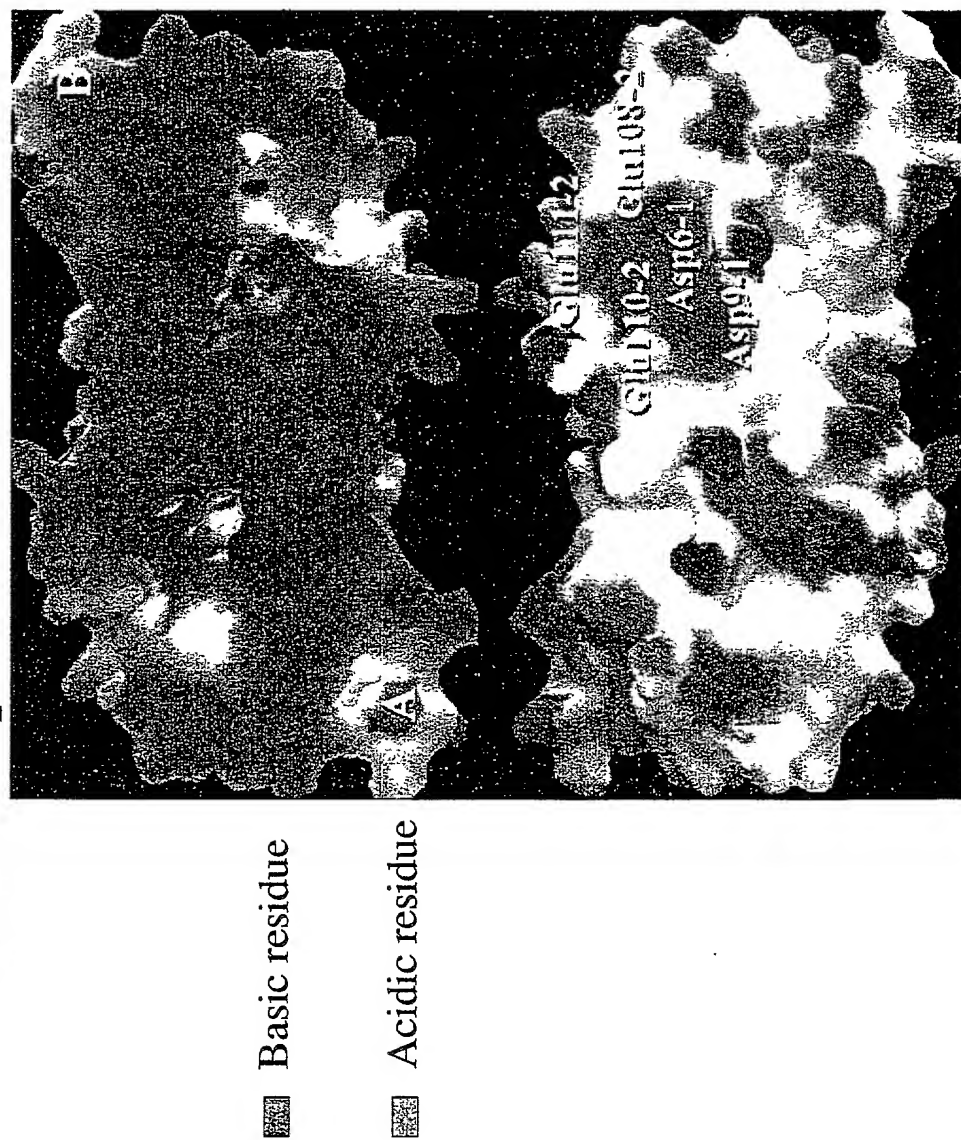
FIG. 11
Alignment of the SarA Homologs



H: residues involved in dimerization, A: acidic residues involved in activation,
D: basic residues involved in DNA binding

FIG. 12 A & B

Electrostatic potential surface of the dimeric SarR structure



The distance from A to B is 71 Angstrom (20 nt) but the inner distance is 92 Angstrom (27 nt)

FIG. 13A

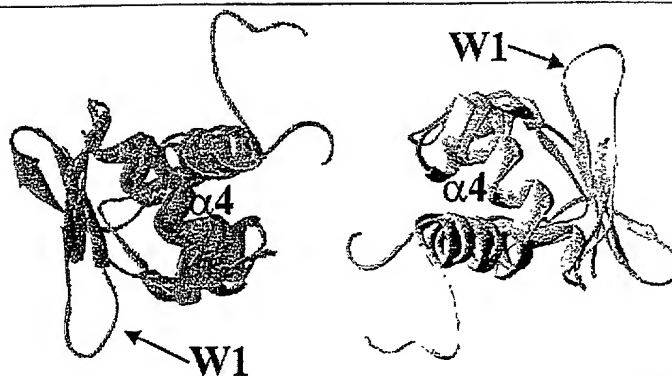


FIG. 13B

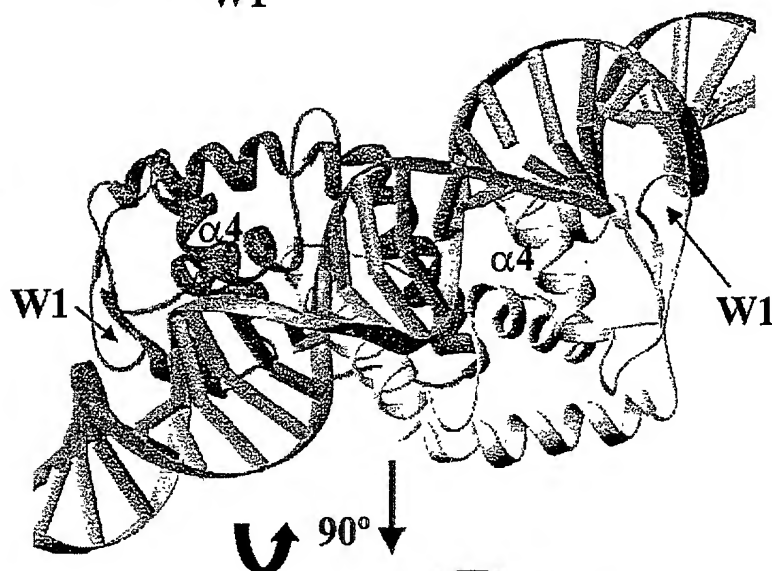


FIG. 13C

